

SEQUENCE LISTING

SEQ ID 1 – NadA from strain 2996, with C-terminus deletion

5 MKHFPSKVLTTAILATFCSGALAATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAADVEADDF
KGLGLKKVVTNLTKTVNENKQNVDAKVKAASEIEKLTTKLADTDAALADTDAALDATTNALNKLGENITTTAEETKTNI
KIDKLEAVADTVDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVKAETAAGKAEAAAGTANTAAD
KAEAVAAKVTDIKADIATNKDNI AKKANSADVTTREESDSKFVRIDGLNATTEKLDTRLASA EKS IADHDTRLNGLDKTVS
DLRKETRQGLAEQAALSGLFQPYNVG

SEQ ID 2 – NadA from strain 2996, with C-terminus deletion and leader peptide processed

10 ATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAADVEADDFKGLGLKKVVTNLTKTVNENKQNV
DAKVKAASEIEKLTTKLADTDAALADTDAALDATTNALNKLGENITTTAEETKTNI VKIDKLEAVADTVDKHAEAFNDI
ADSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVKAETAAGKAEAAAGTANTAADKAEAVAAKVTDIKADIATNKDNI
AKKANSADVTTREESDSKFVRIDGLNATTEKLDTRLASA EKS IADHDTRLNGLDKTVS DLRKETRQGLAEQAALSGLFQPY
NVG

SEQ ID 3 – ΔG741 from MC58 strain

15 VAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAQAQAEKTYGNGDSLNTGKLKNDKVS RFD FIRQIEVDGQL
ITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKVMAKRQFRIGDIA GEHTSF DKLPEGGRATYRGTAFGSDDAGGKLT
IDFAAQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQA EKGSYSLGI FGGKAQEVAGSAEVKTVNGIRHIG
LAAKQ

SEQ ID 4 – 936 from MC58 strain with leader peptide processed

20 VSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETTARSYL RQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQ
IARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQITQKVST
TVGVQKVITLYQNYVQR

SEQ ID 5 – 953 from MC58 strain with leader peptide processed

25 ATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIR
FVSTKFNFGKLVSDGNLTMHGKTAPVKLKA EKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDIQ
IEAAKQ

SEQ ID 6 – ΔG287 from MC58 strain

30 SPDVKSADTL SKPAAPVVSEKETEAKEDAPQAGSQGQAPS AQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN DMPQN
AAGTDSSTPNHTPDNMLAGNMENQATDAGESSQPANQPD MANAADGMQGDDPSAGGQ NAGNTAAQGANQAGNNQAAGSSD
PIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTLTHCKG DSCSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKF
VGLVADSVQMKGINQYII FYKPKPTS FARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYL
TYGAELPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSV DGIIDSGDDLHMGTKQKF
KAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKG GFGVFAGKKEQD

SEQ ID 7 – 287-953 hybrid

35 MASPDVKSADTL SKPAAPVVSEKETEAKEDAPQAGSQGQAPS AQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQN DMP
QNAADTDSLTPNHTPASNPAGNMENQAPDAGESEQ PANQPD MANTADGMQGDDPSAGGENAGNTAAQGTNQAENNTAGS
QNPASSTNPSATNSGGDFGRNTVGNVSVVIDGPSQNTLTHCKG DSCSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKND
GKNDKFVGLVADSVQMKGINQYII FYKPKPTS FARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPE
GNYRYLTYGAELPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSRGRFAAKVDFGSKSV DGIIDSGDGLH
40 MGTQKFKA AIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKG GFGVFAGKKEQD GSGGGGATYKVDEYHA
NARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFG
KKLVSDGNLTMHGKTAPVKLKA EKFNCYQSPMAKTEVCGGDFSTTIDRTKWGV DYL NVNVGMTKSVRIDIQ IEAAKQ*

SEQ ID 8 – 936-741 hybrid

45 MSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETTARSYL RQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVG
QIARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQITQKVS

TTVGVQKVITLYQNYVQRSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAQAQAEKTYGNGDSLNTGKLKNDKVS RFD FIRQ IEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLP
EGGRATYRGTAFGSDDAGGKLTYYTIDFAAKQGNKGIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEGKSYSLGI
FGGKAQEVAGSAEVKTVNGIRHIGLAAKQ*

5 **SEQ ID 9 – linker**

GSGGGG

SEQ ID 10 – 741 sequence

10 CSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAQAQAEKTYGNGDSLNTGKLKNDKVS RFD FIRQ
IEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLP
GGKLTYYTIDFAAKQGNKGIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEGKSYSLGIFGGKAQEVAGSAEVKTV
NGIRHIGLAAKQ

SEQ ID 11 – 741 sequence

15 CSSGGGGVAADIGAGLADALTAPLDHKDKSLQSLTLDQSVRKNEKLKLAQAQAEKTYGNGDSLNTGKLKNDKVS RFD FIRQ
IEVDGQLITLESGEFQIYKQDHS AVVALQIEKINNPDKIDSLINQRSFLVSGLGGEHTAFNQLPDGKAEYHGKAFSSDDAG
GKLTYYTIDFAAKQGHGKIEHLKTPEQNVELAAAELKADEKSHAVILGDTRYGSEEKGTYYHLALFGDRAQEIAGSATVKIGE
KVHEIGIAGKQ

SEQ ID 12 – 741 sequence

20 CSSGGGGSGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEDSIPQNGTLTLSAQGAECTFKAGDKDNLNTGKLKNDKI
SRFDFVQKIEVDGQTITLASGEFQIYKQNHSAVVALQIEKINNPDKTDLSLINQRSFLVSGLGGEHTAFNQLPGGKAEYHGK
AFSSDDPNRLHYSIDFTKKQGYGRIEHLKTLEQNVELAAAELKADEKSHAVILGDTRYGSEEKGTYYHLALFGDRAQEIAG
SATVKIGEKVHEIGIAGKQ